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<b>(54) Title:</b> HUMANIZED ANTIBODIES TO CD38  <b>(57) Abstract</b> <p>The present invention relates to a monoclonal antibody, preferably with specificity for CD38, having CDRs of foreign origin and a recipient framework region having a sequence of human or primate origin, wherein the original amino acid residues in position 29 and/or 78 of the sequence of the recipient framework region of the heavy chain is replaced by a replacement amino acid residue that is the same or similar to that in the corresponding position of the sequence of the corresponding framework region of the heavy chain of the antibody from which the CDRs are derived. Method of preparation of said antibody. Pharmaceutical composition containing said antibody. Use of said antibody for the treatment of cancer and autoimmune diseases.</p>		

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## Humanized antibodies to CD38

The present invention relates to antibodies and in particular to humanised antibodies and their preparation.

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Antibodies typically comprise two heavy chains linked together by disulphide bonds and two light chains. Each light chain is linked to a respective heavy chain by disulphide bonds. Each heavy chain has at one end a variable domain followed by a number of constant domains. Each light chain has a variable domain at one end and a constant domain at its other end. The light chain variable domain is aligned with the variable domain of the heavy chain. The light chain constant domain is aligned with the first constant domain of the heavy chain. The constant domains in the light and heavy chains are not involved directly in binding the antibody to antigen.

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20 The variable domains of each pair of light and heavy chains form the antigen binding site. The variable domains on the light and heavy chains have the same general structure and each domain comprises a framework of four regions, whose sequences are relatively conserved, connected by three complementarity determining regions (CDRs: CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 and CDRH3). The four framework regions largely adopt a beta-sheet conformation and the CDRs form loops connecting, and in some cases forming part of, the beta-sheet structure. The CDRs are held together in close proximity by the framework regions and, with the CDRs from the other domain, contribute to the formation of the antigen binding site. The four framework regions are therefore crucial in ensuring the correct positioning of the CDRs relative to each other and hence in antibody binding.

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The importance of the interaction between the CDRs and the framework regions has become increasingly evident as more and more non-human antibodies have become humanised, such humanised antibodies comprising non-human CDRs  
5 within a human framework. Humanised antibodies, in contrast to non-human antibodies, say mouse or rat antibodies, elicit a negligible immune response when administered to a human.

10 The prior art discloses several ways of producing such humanised antibodies. Thus EP-A-0239400 describes splicing CDRs into a human framework. Briefly, the CDRs are derived from a non-human species such as a rat or mouse whilst the framework regions of the variable  
15 domains, and the constant domains, are derived from a human antibody. Specifically, a humanised anti-CD52 antibody is disclosed in EP-A-0328404.

EP-A-054951 describes another way of humanising an  
20 antibody by re-shaping a non-human antibody to make it more like a human antibody. Basically, it comprises taking a non-human variable domain, such as mouse or rat variable domain, and changing the residues in the framework region to correspond to residues of a human  
25 framework.

In both EP-A-0239400 and EP-A-054951 an altered antibody is produced in which the CDRs of the variable domain of the antibody are derived from a first non-human species  
30 and the framework regions and, if present, the or each constant domain of the antibody are derived from human.

In such humanised antibodies a number of residues of the human framework region appear to exert a critical  
35 influence on the affinity of antigen binding (for example

Kettleborough et al, 1991, Prot. Eng. 4:773). Certain positions in the heavy chain framework regions, in particular, seem to be important in the retention of antigen-binding activity in a variety of altered antibodies. A number of investigators have reported the importance of residues at positions 67, 69 and 71, within the heavy chain framework region. These residues form a beta-sheet in contact with the interior aspect of the CDRH2 loop: presumably mismatches at these positions distort the CDR shape. Also, residues at positions 91 and 94 appear to be important for correct CDRH3 conformation in many heavy chains (for example Tempest et al, Bio/Technology 9:266). Other positions likely to affect antigen-binding are residues 27, 30 and 94 in the heavy chain, and residue 49 and 71 in the light chain (numbering according to the Kabat system). Furthermore, in the heavy chain the importance of regions 66-73 and 27-30 has been recognised in the literature, with residues 66-73 lying in close contact with CDRH2. It has now been found that the residues 29 and 78 of the framework region occupy a pocket which lies close to CDRH1 and affects antigen binding and that this undesirable effect can be obviated by using residues corresponding to those in the corresponding position of the framework region of the antibody from which the CDRs are derived.

Accordingly, the present invention is directed to a monoclonal antibody having donor CDRs of foreign origin and a recipient framework region having a sequence of human or primate origin, wherein the original amino acid residue in position 29 or 78 of the sequence of the recipient framework region of the heavy chain is replaced by a replacement amino acid that is the same or similar to that in the corresponding position of the sequence of

the corresponding framework region of the antibody from which the CDRs are derived. By "similar" is meant an amino acid of equivalent size preferably of equivalent size, hydrophobicity and charge.

5

Typically, the original amino acid residues in positions 29 and/or 78 of the recipient framework region are larger than their corresponding residues in the framework region of the antibody from which the CDRs are derived.

10 Examples of these larger residues include tyrosine, histidine, tryptophan and 2-phenylalanine. Examples of the smaller corresponding residues in the framework region of the antibody donating the CDRs include glycine, alanine, valine, serine and leucine. In accordance with  
15 the invention, the larger original residue in positions 29 and/or 78 of the recipient framework is replaced with a replacement amino acid residue that is either the same or similar to the corresponding smaller residue of the antibody which is donating the CDRs.

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Although it is preferable for the replacement amino acid residue to be the same as the corresponding residue of the antibody which is donating the CDRs it can also be a similar amino acid residue provided the character with  
25 respect to size and preferably also hydrophobicity and charge is essentially the same i.e. conserved. For example, if the residue of the antibody which is donating the CDRs has a valine in position 29 and/or 78, then instead of having a replacement amino acid residue in the  
30 recipient framework which is also valine, one could, for example, use alanine instead since alanine is of equivalent charge, size and hydrophobicity to valine and thus similar. The use of a similar amino acid in place of the exact same amino acid is a practice which is well  
35 established in the art and known as conservative

substitution.

By way of example, in a mouse heavy chain framework, side chains of Leu-29 and Val-78 would pack together in a small pocket close to CDRH1 whilst in the corresponding human heavy chain framework, such as for example NEW, which otherwise bears close homology to the mouse framework, the analogous positions are occupied by two Phe residues. The large aromatic side-chains appear to be too bulky to pack in the same fashion as in the mouse antibody and so alter the disposition of neighbouring surface residues resulting in a different conformation of CDRH1 in a humanised antibody. Substituting either Phe residue by the smaller murine residue partially relieves this effect allowing antigen binding. Full affinity is generally restored by replacement of both residues. It is therefore preferred that amino acids in both positions 29 and 78 are replaced.

In accordance with the invention, the replacement amino acid residues fit into the pocket without causing distortion of, for example, the CDRH1 conformation.

Preferably, the framework of the antibody heavy chain is homologous to the corresponding framework of the human antibody NEW (Saul et al, J. Biol. Chem. 253:585-597, 1978). The final residue of framework 1 in this case is suitably Ser or Thr, preferably Ser. This residue is at position 30 (Kabat et al, 1987). Preferably the framework of the antibody light chain is homologous to the variable domain framework of the protein REI (Epp et al, Eur. J. Biochem., 45:513-524, 1974).

Particular examples of murine heavy chains in which residues 29 and 78 pack together in a small pocket close

to CDRH1 are those in Kabat groups IB and IIC.

By contrast, other examples of human heavy chains which have bulky residues in positions 29 and 78 in the framework region are LES-C, T52, Ab44, HIgI and NEW, as listed in Kabat.

Species other than the mouse that may have residues of a small size in positions 29 and 78 are for example, the rat, rabbit and hamster.

All amino acid residue positions referred to herein employ the Kabat numbering system.

An antibody according to the invention may be produced by a method including the steps of:

- (i) obtaining the sequence of a donor heavy chain;
- (ii) selecting a recipient human or primate framework by best-fit homology method;
- (iii) replacing the amino acid residue in position 29 or 78 of the sequence of the recipient framework region of the heavy chain by an amino acid that is the same or similar to that in the corresponding position of the sequence of the corresponding framework region of the antibody from which the CDRs are derived.

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The antibody heavy chain may be co-expressed with a complementary antibody light chain. At least the framework regions of the variable domain and the or each constant domain of the complementary chain generally are derived from the primate or human recipient. Preferably

35



the CDRs of both chains are derived from the same selected antibody.

The antibody preferably has the structure of a natural  
5 antibody or a fragment thereof. The term antibody may  
therefore comprise a complete antibody, a (Fab')<sub>2</sub>  
fragment, a Fab fragment, Fv fragment, Fd fragment, SFv,  
a light chain dimer or a heavy chain and derivatives  
thereof. The antibody may be an IgG such as an IgG1,  
10 IgG2, IgG3 or IgG4, IgM, IgA, IgE or IgD. Furthermore,  
the antibody may comprise modifications of all classes  
e.g. IgG dimers, Fc mutants that no longer bind Fc  
receptors or mediate Clq binding (blocking antibodies).  
The antibody may also be a chimeric antibody of the type  
15 described in WO 86/01533) which comprises an antigen  
binding region and a non-immunoglobulin region. The  
antigen binding region is an antibody light chain  
variable domain or heavy chain variable domain.  
Typically, the antigen binding region comprises both  
20 light and heavy chain variable domains. The non-  
immunoglobulin region is fused at its C-terminus to the  
antigen binding region. The non-immunoglobulin region  
is typically a non-immunoglobulin protein and may be an  
enzyme, a toxin or a protein having known binding  
25 specificity. The two regions of the chimeric antibody  
may be connected via a cleavable linker sequence.

The invention is preferably employed to humanise an  
antibody, for example, an antibody of rat, rabbit,  
30 hamster or mouse origin. The framework regions and  
constant domains of the humanised antibody are therefore  
of human or primate origin whilst the CDRs of the light  
and/or heavy chain of the antibody are for example, rat  
or mouse CDRs. The antibody may be a human or primate  
35 IgG such as IgG1, IgG2, IgG3, IgG4; IgM; IgA; IgE or IgD

in which the CDRs are of rat or mouse origin.

The antibody from which the donor CDRs are derived is typically an antibody of a selected specificity. In order to ensure that this specificity is retained, either the variable domain framework regions of the antibody are re-shaped to correspond to variable domain framework regions of a human or primate antibody or the CDRs are grafted onto the closest human or primate framework regions. Either way, the resulting antibody preferably comprises non-human CDRs and human or primate framework regions that are homologous with the corresponding framework regions of the antibody from which the CDRs are derived. Preferably there is a homology of at least 50% between the two variable domains.

There are four general steps to produce a humanised antibody. These are:

- (1) determining the nucleotide and predicted amino acid sequence of the light and heavy chain variable domains of the antibody from which the CDRs are derived;
- (2) deciding which human or primate antibody framework region to use;
- (3) the actual grafting or re-shaping methodologies/ techniques; and
- (4) the transfection and expression of the grafted or re-shaped antibody.

These four steps are explained below.

Step 1: Determining the nucleotide and predicted amino acid sequence of the antibody light and heavy chain variable domains

5 To humanise an antibody the amino acid sequence of the non-human antibody's (donor antibody's) heavy and light chain variable domains needs to be known. The sequence of the constant domains is irrelevant. The simplest method of determining an antibody's variable domain amino  
10 acid sequence is from cloned cDNA encoding the heavy and light chain variable domain.

There are two general methods for cloning a given antibody's heavy and light chain variable domain cDNAs:  
15 (1) via a conventional cDNA library, or (2) via the polymerase chain reaction (PCR). Both of these methods are widely known. Given the nucleotide sequence of the cDNAs, it is a simple matter to translate this information into the predicted amino acid sequence of the  
20 antibody variable domains.

Step 2: Designing the humanised antibody

25 There are several factors to consider in deciding which human antibody (recipient antibody) sequence to use during humanisation. The humanisation of light and heavy chains are considered independently of one another, but the reasoning is basically the same.

30 This selection process is based on the following rationale: A given antibody's antigen specificity and affinity is primarily determined by the amino acid sequence of the variable region CDRs. Variable domain framework residues have little or no direct contribution.  
35 The primary function of the framework regions is to hold

the CDRs in their proper spacial orientation to recognise the antigen. Thus the substitution of rodent CDRs into a human variable domain framework is most likely to result in retention of the correct spacial orientation if the human variable domain is highly homologous to the rodent variable domain from which the CDRs were derived. A human variable domain should preferably be chosen therefore that is highly homologous to the rodent variable domain(s).

10

A suitable human antibody variable domain sequence can be selected as follows:

- (i) Using a computer program, search all available protein (and DNA) databases for those human antibody variable domain sequences that are most homologous, for example, to the rodent antibody variable domains. This can be easily accomplished with a program called FASTA but other suitable programs are available. The output of the program is a list of sequences most homologous to the rodent antibody, the percent homology to each sequence, and an alignment of each sequence to the rodent sequence. This is done independently for both the heavy and light chain variable domain sequences. The above analyses are more easily accomplished if customised sub-databases are first created that only include human immunoglobulin sequences. This has two benefits. First, the actual computational time is greatly reduced because analyses are restricted to only those sequences of interest rather than all the sequences in the databases. The second benefit is that, by restricting analyses to only human immunoglobulin

sequences, the output will not be cluttered by the presence of rodent immunoglobulin sequences. There are far more rodent immunoglobulin sequences in databases than there are human.

5

(ii) List the human antibody variable domain sequences that have the most overall homology to the rodent antibody variable domain (from above). Do not make a distinction between homology within the framework regions and CDRs. Consider the overall homology.

10

(iii) Eliminate from consideration those human sequences that have CDRs that have a different length than those of the rodent CDRs. This rule does not apply to CDR 3, because the length of this CDR is normally quite variable. Also, there are sometimes no or very few human sequences that have the same CDR lengths as that of the rodent antibody. If this is the case, this rule can be loosened, and human sequences with one or more differences in CDR length can be allowed.

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(iv) From the remaining human variable domains, one is selected that is most homologous to that of the rodent.

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(v) The actual humanised antibody (the end result) should contain CDRs derived from the rodent antibody and a variable domain framework from the human antibody chosen above.

30

(vi) Instead of re-shaping or grafting to produce a humanised antibody, it would also be possible to synthesise the entire variable domain from

35

scratch once the amino-acids of the non-human variable domain has been determined and the most homologous human variable domain has been identified.

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(vii) If donor heavy chain has two small residues at positions 29 and 78, and recipient chain has large, typically aromatic, residues at one or both of these positions, then further analysis is required.

10

(viii) This analysis may take the form of a sequence comparison between the CDRH1 of the donor chain and that of other antibodies. For example, a CDRH1 sequence of SYGVH has been shown to require small residues at positions 29 and 78 for complete activity, and it is to be expected that other antibodies with the same or similar CDRH1 sequence will also require residues at these positions.

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Alternatively, the analysis may take the form of detailed computer aided modelling of the CDRH1 region of the proposed humanised antibody using standard techniques (for example the *AbM* package from Oxford Molecular Ltd). If this analysis, for example, reveals that CDRH1 lies in close approximation to the packed side chains of residues 29 and 78, and that altering these residues from human to smaller residues changes the orientation or position of CDRH1, then such smaller residues should replace the human ones. An example of such a perturbation of CDRH1 is shown in Figures 5 and 6.

35

Step 3: Grafting and re-shaping

See EP-A-0239400 and EP-A-054951 for details.

5    Step 4: The transfection and expression of the altered  
          antibody

Once the antibody has been humanised and residues 29  
and/or 78 replaced, the cDNAs are linked to the  
10    appropriate DNA encoding light or heavy chain constant  
region, cloned into an expression vector, and transfected  
into mammalian cells. These steps can be carried out in  
routine fashion. A humanised antibody may therefore be  
prepared by a process comprising:

- 15    (a) preparing a first replicable expression vector  
          including a suitable promoter operably linked to a  
          DNA sequence which encodes at least a variable  
          domain of an Ig heavy or light chain, the variable  
20    domain comprising framework regions from a human or  
          primate antibody and CDRs comprising at least parts  
          of the CDRs from a second antibody of different  
          origin;
- 25    (b) if necessary, preparing a second replicable  
          expression vector including a suitable promoter  
          operably linked to a DNA sequence which encodes at  
          least the variable domain of a complementary Ig  
          light or heavy chain respectively;
- 30    (c) transforming a cell line with the first or both  
          vectors; and
- 35    (d) culturing said transformed cell line to produce  
          said altered antibody.

Preferably the DNA sequence in step (a) encodes both the variable domain and the or each constant domain of the antibody chain, the or each constant domain being derived from the human or primate antibody. The antibody can be recovered and purified. The cell line which is transformed to produce the altered antibody may be a Chinese Hamster Ovary (CHO) cell line or an immortalised mammalian cell line, which is advantageously of lymphoid origin, such as a myeloma, hybridoma, trioma, or quadroma cell line. The cell line may also comprise a normal lymphoid cell, such as a B-cell, which has been immortalised by transformation with a virus, such as the Epstein-Barr virus. Most preferably, the immortalised cell line is a myeloma cell line or a derivative thereof.

Although the cell line used to produce the altered antibody is preferably a mammalian cell line, any other suitable cell line, such as a bacterial cell line or a yeast cell line, may alternatively be used. In particular it is envisaged that E. coli-derived bacterial strains could be used.

Some immortalised lymphoid cell lines, such as myeloma cell lines, in their normal state secrete isolated Ig light or heavy chains. If such a cell line is transformed with the vector prepared in step (a), it may not be necessary to carry out step (b) of the process, provided that the normally secreted chain is complementary to the variable domain of the Ig chain encoded by the vector prepared in step (a). However, where the immortalised cell line does not secrete a complementary chain, it will be necessary to carry out (b). This step may be carried out by further manipulating the vector produced in step (a) so that this vector encodes not only the variable domain of an altered



antibody light or heavy chain, but also the complementary variable domain.

Alternatively, step (b) is carried out by preparing a second vector which is used to transform the immortalised cell line. This alternative leads to easier construct preparation, but may be less preferred than the first alternative in that it may not lead to as efficient production of antibody.

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Where the immortalised cell line secretes a complementary light or heavy chain, the transformed cell line may be produced for example by transforming a suitable bacterial cell with the vector and then fusing the bacterial cell with the immortalised cell line by spheroplast fusion. Alternatively, the DNA may be directly introduced into the immortalised cell line by electroporation or other suitable method.

20 The present process has been applied to obtain an antibody against the CD38 surface antigen.

Briefly, a humanised anti-CD38 monoclonal antibody (termed h3S) was produced in the following fashion. cDNA was obtained from hybridoma cells secreting the murine monoclonal anti-(human CD38) AT13/5. cDNA clones encoding the heavy and light chains of the mouse antibody were identified and sequenced (Sequences 1 and 2 attached in Figures 1 and 2). This information was then used to choose appropriate human frameworks to receive the CDR grafts by the best-fit homology method. This procedure identified the REI light chain and the NEW heavy chain as the optimal choices.

35 CDRs were grafted on to the human frameworks. In

addition, guided by published work (Riechman et al., 1988 Nature 332: 323 and Tempest et al., 1991, Bio/Technology 9:266), four framework changes were made at this stage at positions likely to affect antigen-binding: residues  
5 27,30 and 94 in the heavy chain, and residue 49 in the light chain (numbering according to the Kabat system). The resulting humanised antibody was tested for CD38 binding, with negative results. Expression of the humanised light chain together with a chimeric heavy  
10 chain (murine VH, human CH) produced functional antibody, indicating that the humanisation of the light chain was adequate.

A further series of heavy chain framework changes were  
15 examined. In particular, the analysis identified a stretch of sequence from residue 66 to 73 which lies in close contact with CDRH2 and a pocket formed by the side chains of residues 29 and 78, lying close to CDRH1, as affecting antigen binding. As mentioned earlier on the  
20 importance of the regions 66-73 and 27-30 is recognised in the literature, though the role of residue 29 and 78 and the interaction between the side chains of residues 29 and 78 is not.

25 Although the invention is described with reference to an anti-CD38 antibody it is applicable to any antibody, whatever antigen it binds to. In particular any antibodies that bind the 40kD antigen (CO/17.1.A) as disclosed in J. Cell. Biol., 125 (2) 437-446, April 1994  
30 and in Proc. Natl. Acad. Sci. 87, 3542-3546, May 1990, carcinoma antigens and antigens involved in autoimmune diseases. A specific example of an anti-40KD antibody is 323/A3.

35 Another example of an antibody is an anti-folate receptor

antibody as disclosed in A. Tomasetti et al, Federation of European Biochemical Societies Vol 317, 143-146, Feb 1993. A specific example of an anti-folate antibody is MOV18. Further examples of antibodies include anti-CEA,  
5 anti mucin, anti-20/200KD, anti-ganglioside, anti-digoxin, anti-CD4 and anti-CD23.

In particular the anti-CD38 antibody has the nucleotide sequences for the heavy chain and light chain variable  
10 region as shown in Figures 3, 3a and 4.

According to another aspect of the present invention there is provided the use of antibody according to the present invention in therapy. In particular there is  
15 provided the use of antibodies according to the invention for the treatment of cancer and their associated metastases and for treatment of autoimmune diseases, in particular for the treatment of multiple myeloma, lymphoma and rheumatoid arthritis.

20 The anti-CD38 antibody of the present invention can be used in the treatment of multiple myeloma.

CD38 is a transmembrane glycoprotein expressed by  
25 immature B lymphocytes, activated T and B lymphocytes, and plasma cells. Antibodies to CD38 capable of causing cell lysis may be useful in the immunotherapy of tumours bearing this antigen, principally multiple myeloma and 50% of non-Hodgkin's lymphomas. Additionally, anti-CD38  
30 antibodies may be useful in the treatment of autoimmune diseases such as rheumatoid arthritis and myaethenia gravis, as they have the potential to suppress both the humoral and cellular effector arms of the immune system.

35 A CD38 antibody according to the present invention has

been demonstrated to be lytic for cells expressing CD38 on their surface. The humanised antibody has been shown to bind CD38 and compete with the parental antibody in CD38 binding.

5

Multiple myeloma is a neoplasm characterised by an accumulation of a clone of plasma cells, frequently accompanied by the secretion of immunoglobulin chains. Bone marrow invasion by the tumour is associated with  
10 anaemia, hypogammaglobinaemia and granulocytopaenia with concomitant bacterial infections. An abnormal cytokine environment, principally raised IL6 levels, often results in increased osteoclasts leading to bone pain, fractures and hypercalcaemia. Renal failure is not uncommon in the  
15 context of high concentrations of myeloma immunoglobulin and hypercalcaemia.

A variety of therapeutic protocols have been tried over recent years with little impact on the overall prognosis  
20 for myeloma patients. Treatment with melphalan and prednisolone remains the standard therapy, as it was thirty years ago (Bergsagel, 1989). A response to chemotherapy is associated with the induction of remission with median duration of about two years, but  
25 in all cases this is followed by eventual relapse and death (Alexanian and Dimopoulos, 1994 New England J. of Medicine Vol. 330 : 484). More aggressive chemotherapy utilising multiple cytotoxic agents has yielded little additional benefit in terms of survival or duration of  
30 remission, though high-dose therapy followed by autologous bone marrow transplant remains an area of active development.

Several workers have proposed immunotherapeutic  
35 strategies to combat myeloma. Interleukin 6 has been

suggested to be a major growth factor for myeloma cells and may function in either an autocrine or paracrine fashion. Based on such results, interventions aimed at disrupting the IL6 signalling system have been designed.

5 Two murine monoclonal that neutralise IL6 suppressed the proliferation of myeloma cells in a patient with leukaemic variant of the disease, though the tumour relapsed after 60 days.

10 Administration of anti-IL6 receptor monoclonal antibody to SCID mice engrafted with cells from a human myeloma cell line suppressed tumour growth, though only if the antibody was administered one day after injection of the myeloma cells. Antibody given after five days of growth

15 had no significant effect. A CDR-grafted form of this antibody has also been prepared for possible human therapeutic use.

In a similar vein, myeloma cells bearing high levels of

20 IL6 receptor have also been targeted by chimeric cytotoxins consisting of IL6 variants linked to a modified form of Pseudomonas exotoxin. Cell killing is seen in vitro though the applicability of this technique in the clinic remains to be seen.

25 Our preference is for a more physiological approach, targeting myeloma cells for killing by the host immune system. The surface antigen CD38 is strongly expressed by more than 90% of multiple myeloma cells, and its

30 suitability as a target for lytic immunotherapy has been discussed (Stevenson et al, 1991 Blood, Vol. 77, 5 : 1071-1079). The same report also demonstrated the competence of effector cells from myeloma patients for lysis of target cells coated with a chimeric anti-CD38.

The dosages of such antibodies will vary with the condition being treated and the recipient of the treatment, but will be in the range 1 to about 100 mg for an adult patient, preferably 1 - 10 mg, usually  
5 administered daily for a period between 1 and 30 days. A two part dosing regime may be preferable wherein 1 - 5 mg are administered for 5 - 10 days followed by 6 - 15 mg for a further 5 - 10 days.

10 Also included within the invention are formulation containing a purified preparation of an anti-CD38 antibody. Such formulation preferably include, in addition to antibody, a physiologically acceptable  
15 diluent or carrier possibly in admixture with other agents such as other antibodies or antibiotic. Suitable carriers include but are not limited to physiological saline, phosphate buffered saline, phosphate buffered saline glucose and buffered saline. Alternatively, the  
20 antibody may be lyophilised (freeze-dried) and reconstituted for use when needed, by the addition of an aqueous buffered solution as described above. Routes of administration are routinely parenteral including intravenous, intramuscular, subcutaneous and intraperitoneal injection or delivery.

25 The following Examples illustrate the invention. In the accompanying drawings:

30 Figure 1 shows the nucleotide and predicted amino acid sequence of mouse anti-CD38 antibody heavy chain variable region. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. CDRs are underlined.

35 Figure 2 shows the nucleotide and predicted amino acid

sequence of mouse anti-CD38 antibody light chain variable region. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins respectively. CDRs (underlined) were  
5 identified by comparison to known immunological sequences (Kabat *et al*, "Sequences of proteins of immunologic interest", US Dept of Health and Human Services, US Government Printing Office, 1987).

10 Figures 3 and 3a together show the nucleotide and predicted amino acid sequence of the humanised anti-CD38 antibody light chain cDNA. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. CDRs are  
15 underlined.

Figure 4 shows the nucleotide and predicted amino acid sequence of the humanised anti-CD38 antibody heavy chain cDNA. The number of the first and last amino acid or  
20 nucleotide in each line is indicated in the left and right margins, respectively. CDRs are underlined.

Figure 5 shows the configuration of the CDRHI (dark tubes) in the murine-anti-CD38 (murine residues at  
25 positions 29 and 78).

Figure 6 shows the configuration of the CDRHI (dark tubes) in the same region as Figure 5, but in a humanised construct with human residues at positions 29 and 78.

30 Figure 7 shows the effect of various heavy chain framework substitutions on relative binding affinity of anti-CD38 antibodies.

35 Figure 8 shows the effect of various heavy chain

framework substitutions on antibody dependent cellular cytotoxicity mediated by CD38 antibodies.

### Examples

5

#### Example 1

#### Humanisation of anti-CD38 based on a mouse antibody (AT13/5:IqGLK)

10

##### (a) General note on methodology

Unless otherwise stated, in the methodology described below, the following standard procedures and conditions were used. Manufacturers' recommended protocols were followed where applicable.

PCR experiments (Saiki et al, Science 239:487-491, 1988) were conducted using a programmable thermal cycler (Trio Biometra). A typical 100µl reaction mix contained 2.5 units of AmpliTag polymerase (Perkin-Elmer Cetus, Beaconsfield, UK) in the buffer supplied by the manufacturer; 250µM of each of dATP, dCTP, dGTP and dTTP, amplification primers at 1 µM, and template DNA. Unless otherwise noted, the following cycle specifications were used:

step 0: 94°C for 90 seconds  
step 1: 94°C for 60 seconds  
30 step 2: 50°C for 60 seconds, ramping up to step 3 at a rate of 0.15°C/second  
step 3: 72°C for 60 seconds, go to step 1, repeating this loop for 25 cycles  
step 4: 72°C for 10 minutes.

35



DNA sequencing was performed by the dideoxy method using the Sequenase v2 system (USB, Cambridge, UK), according to the manufacturer's instructions. The reaction products were separated on 8% acrylamide sequencing gels  
5 (Gel-Mix 8, BRL, Paisley, Scotland, UK).

To gel-purify DNA, one of two methods was used. For fragments smaller than 175 base-pairs, the DNA was separated on a conventional high-melting point agarose gel, and the DNA recovered using the Prep-a-Gene system  
10 (Bio-Rad Laboratories, Hemel Hempstead, UK). Larger fragments were purified by separation on a low-melting point agarose gel (NuSieve GTG, FMC, Rockland, ME), and the DNA recovered using Magic PCR Preps (Promega,  
15 Southampton, UK).

Numbering of amino-acid residues in antibody chains follows the scheme of Kabat et al ("Sequences of proteins of immunological interest", US Dept of Health and Human  
20 Services, US Government Printing Office, 1991).

(b) Cloning and Sequencing of AT 13/5 antibody - Heavy Chain

25 Polyadenylated RNA was extracted from a culture containing  $5 \times 10^6$  of the AT13/5 mouse hybridoma line using a Micro Fast Tract kit (British Biotechnology, Oxford, UK). This was converted into oligo-dT-primed single-stranded cDNA using the SuperScript  
30 Preamplification system (BRL, Paisley, Scotland, UK). Aliquots of the resulting cDNA were used in PCRs designed to separately amplify the variable region of mouse immunoglobulin heavy and light chains.

35 The variable region of the heavy chain was amplified

according to the method of Jones & Bendig (Bio/Technology 9:88-89), using a cocktail of primers specific to the signal peptide region (MHV1-12) and one primer specific for the mouse  $\gamma 1$  constant region (Mouse IgG1 heavy chain reverse primer). The resulting PCR fragment was digested with Xma I and Sal I and cloned into pUC18. Clones obtained from two independent PCR reactions were sequenced on both strands and found to be identical implying that the sequence does not contain errors introduced by the PCR process. The complete sequence of the variable region appears as Figure 1.

(c) Cloning and Sequencing of AT13/5 antibody - Light Chain

The sequence of the variable region of the light chain was also derived by a PCR-based cloning strategy using the same preparation of single-stranded cDNA as for the heavy chain. However, a more complex cloning and sequencing protocol was required, as the primers described by Jones & Bendig (*op cit*) preferentially amplify a non-productively rearranged kappa light chain from the AT13/5 cDNA. This chain arises from the fusion partner used to generate the AT13/5 hybridoma, here termed the MOPC-21 related  $V_{\kappa}$ , and is of known sequence (Carroll, WL et. al., Molecular Immunology 25:991-995; 1988).

To amplify the cDNA encoding the anti-CD38 light chain a PCR was performed using the mouse kappa light chain reverse primer described by Jones & Bendig (*op cit*), and a primer VK1-BACK that hybridises to the framework 1 region of most mouse kappa chains (sequences: 5' GACATTCAGCTGACCCAGTCTCCA 3'). Conditions were as described for the heavy chain amplifications above,

except that 35 cycles were used. These primers do not amplify the cDNA encoding the MOPC-21 related VK under these conditions.

5 An amplification fragment of the appropriate size was purified and a portion of this DNA used as the template for a second amplification (conditions as above, 30 cycles) using the light chain reverse primer and a variant of VK1-BACK containing a Hind III site (sequence:  
10 5' GATCAAGCTTGACATTGACCTGACCCAGTCTCCA 3'). The resulting fragment was digested with Hind III and Xma I and cloned into a pUC18. Clones were sequenced on both strands by the conventional dideoxy method. Additionally, a portion of the PCR product was directly sequenced using a thermal  
15 cycling strategy (fmol system, Promega, Southampton, UK) with a primer (light chain reverse primer, as above) end-labelled with <sup>32</sup>P. The sequence obtained from the cycle sequencing experiment matched exactly the sequence derived by conventional methods.

20

Since this sequence was obtained from the products of two rounds of amplification, further confirmation of its accuracy was sought. The existing light chain sequence was used to design a primer that hybridises to the  
25 framework 1 region (sequence: 5' ACTAGTCGACCATCCTCCTTTCTGTTTCTCTAGGAG 3'). This was used in conjunction with the light chain reverse primer in a PCR with the following cycle definition:

30 step 0: 95°C for 120 seconds  
step 1: 95°C for 60 seconds  
step 2: 50°C for 60 seconds  
step 3: 72°C for 60 seconds, go to step 1, repeating this loop for 30 cycles  
35 step 4: 72°C for 10 minutes

Three independent reactions were performed, and after purification, the products were digested by Xma I and Sal I, and cloned into pUC18. Several clones were sequenced by the dideoxy method. All sequences so obtained were  
5 identical to those obtained previously, confirming that the proposed light chain sequence was indeed free from PCR errors. The complete sequence of the variable region of the light chain appears as Figure 2.

10 (d) Design and construction of version 1 of the humanised antibody

Human variable domain frameworks were selected by the best-fit homology method (Lewis, AP & Crowe, JS in  
15 "Generation of Antibodies by Cell and Gene Immortalisation", Terhorst, C, Malavasi, F, Albertini, A (eds) Karger: Basel, 1993). The frameworks chosen for humanisation process were the light and heavy chain variable domains of Campath 1H (disclosed in EP-A-  
20 0328404). The humanised heavy and light chains were then constructed by a recombinant PCR technique (Lewis & Crowe, Gene 101:297-302, 1991).

i) Light Chain

25

The primers used in the humanisation process were:

A<sub>L</sub>: 5' GATCAAGCTTCTCTACAGTTACTGAGCAC3'  
B<sub>L</sub>: 5' CCGATTATATATGTCCTCACTTGCCTTACAGGTGATGGTCAC3'  
30 C<sub>L</sub>: 5' AGTGAGGACATATATAATCGGTTAACCTGGTACCAGCAGAAG3'  
D<sub>L</sub>: 5' AGTTTCCAACTGGTTGCACCAGAGATCAGCAGCTTTGG3'  
E<sub>L</sub>: 5' GGTGCAACCAGTTTGGAACTGGTGTGCCAAGCAGA3'  
F<sub>L</sub>: 5' GTACGGATTACTCCAATACTGTTGGCAGTAGTAGGTGGC3'  
G<sub>L</sub>: 5' CAGTATTGGAGTAATCCGTACACGTTCCGGCCAAGGGACC3'  
35 H<sub>L</sub>: 5' GATCAAGCTTCTAACACTCTCCCCTGTTGA3'

Primers A<sub>L</sub> and H<sub>L</sub> contain Hind III sites to allow cloning of the final amplification product. PCRs were performed according to the following cycle specification:

- 5    step 0: 95°C for 120 seconds
- step 1: 95°C for 60 seconds
- step 2: 45°C for 60 seconds
- step 3: 72°C for 60 seconds, go to step 1, repeating this
- loop for 25 cycles
- 10   step 4: 72°C for 10 minutes

The template used in this reaction was DNA encoding the Campath 1H light chain, a construct in which the framework residues are taken from REI and the CDRs from a rat anti-human CDw52 antibody (Reichmann, L. *et. al.* Nature 332:323-337, 1988). The primers above are designed to wholly replace the Campath 1H sequence, leaving the AT13/5 CDRs grafted onto the REI frameworks.

- 20   Four initial PCRs were performed using 10ng of template with the primer pairs: A<sub>L</sub> and B<sub>L</sub>, C<sub>L</sub> and D<sub>L</sub>, E<sub>L</sub> and F<sub>L</sub>, and G<sub>L</sub> and H<sub>L</sub>. The products of these reactions, AB<sub>L</sub>, CD<sub>L</sub>, EF<sub>L</sub> and GH<sub>L</sub> respectively were gel-purified and half of the amount recovered used in the second round of PCRs.
- 25   Fragments AB<sub>L</sub> and CD<sub>L</sub> were used as template with primers A<sub>L</sub> and D<sub>L</sub> in one reaction, and fragments EF<sub>L</sub> and GH<sub>L</sub> were used as template with primers E<sub>L</sub> and H<sub>L</sub>. The reaction conditions were:

- 30   step 0: 95°C for 120 seconds
- step 1: 95°C for 60 seconds
- step 2: 45°C for 60 seconds
- step 3: 72°C for 90 seconds, go to step 1, repeating this
- loop for 20 cycles

The products of these reactions, AD<sub>L</sub> and EH<sub>L</sub>, were gel-purified and half of each DNA used as template in a final reaction with primers A<sub>L</sub> and H<sub>L</sub> with the reaction conditions as for the second round PCR above. The  
5 resulting product was digested with Hind III and cloned into pUC18. A clone with the predicted structure as determined by complete sequence of the insert on both strands was chosen for further manipulation. The  
10 sequence of the variable region of this construct is given as Figures 3 and 3a.

ii) Heavy Chain

The primers used in the humanisation process were:

15 A<sub>H</sub>: 5' GATCAAGCTTTACAGTTACTCAGCACACAG3'  
B<sub>H</sub>: 5' GTGGACACCATAACTGGTGAAGGTGAAGCC3'  
C<sub>H</sub>: 5' AGTTATGGTGTCCACTGGGTGAGACAGCCA3'  
D<sub>H</sub>: 5' TTGTAGTCTGTGCTTCCACCTCTCCACATCACTCCAATCCACTCAAG3'  
E<sub>H</sub>: 5' GAAGCACAGACTACAATGCAGCTTTCATGTCCAGAGTGACAATGCTG3'  
20 F<sub>H</sub>: 5' GGAGTCCATCACGAAGCCGGTCGTTATCATGGATTTTGCACAATAATAGAC3'  
G<sub>H</sub>: 5' AAATCCATGATAACGACCGGCTTCGTGATGGACTCCTGGGGTCAAGGCTC  
ACTAGTCACAGTCTCCTCAGCC3'  
H<sub>H</sub>: 5' TAGAGTCCTGAGGGAATTCGGACAGCCGGAAGGTG3'

25

PCRs were performed according to the following cycle specification:

step 0: 95°C for 120 seconds  
30 step 1: 95°C for 60 seconds  
step 2: 45°C for 60 seconds  
step 3: 72°C for 60 seconds, go to step 1, repeating this loop for 25 cycles  
step 4: 72°C for 10 minutes

35

The template used in this reaction was DNA encoding the Campath 1H heavy chain, a construct in which the CDRs and framework residues 27 and 30 are taken from a rat anti-human CDw52 antibody (Reichmann, L *et. al.* op cit), and the remainder of the framework residues from NEW. The primers above are designed to replace the Campath 1H CDR sequences, leaving the AT13/5 CDRs grafted onto the Campath 1H framework. Also, heavy chain residue 94 is known to be important in antigen-binding (Tempest, PR *et. al.*, Bio/Technology, 9:260-271, 1991), so the AT13/5 sequence was adopted at this position. The rat sequence at residues 27 and 30 is more homologous to the AT13/5 sequence than is the unmodified NEW sequence. Primers A<sub>H</sub> and H<sub>H</sub> contains Hind III and EcoR I sites respectively. Additionally, primer G<sub>H</sub> engineers a SpeI site into the framework 4 region to allow coupling to a previously prepared human C<sub>H</sub> sequence.

Four initial PCRs were performed using 10ng of template with the primer pairs: A<sub>H</sub> and B<sub>H</sub>, C<sub>H</sub> and D<sub>H</sub>, E<sub>H</sub> and F<sub>H</sub>, and G<sub>H</sub> and H<sub>H</sub>. The products of these reactions, AB<sub>H</sub>, CD<sub>H</sub> were used as template with primers A<sub>H</sub> and D<sub>H</sub> in one reaction, and fragments EF<sub>H</sub> and GH<sub>H</sub> were used as template with primers E<sub>H</sub> and H<sub>H</sub>. The reaction conditions were:

step 0: 95°C for 120 seconds  
step 1: 95°C for 60 seconds  
step 2: 45°C for 60 seconds  
step 3: 72°C for 90 seconds, go to step 1, repeating this loop for 20 cycles

The products of these reactions, AD<sub>H</sub> and EH<sub>H</sub>, were gel-purified and half of each DNA used as template in a final reaction with primers A<sub>H</sub> and H<sub>H</sub> with the reaction conditions as for the second round PCR above. The

resulting product was digested with Hind III and Spe I, and the fragment containing the variable region cloned into a pUC18-based vector containing the human C<sub>H</sub> sequence. A clone with the predicted structure as  
5 determined by complete sequencing of the insert on both strands was chosen for further manipulation.

(e) Eukaryotic expression of version 1 of the humanised antibody

10

Humanised AT13/5 heavy and light chains were cloned into eukaryotic expression vectors under human  $\beta$  actin promoters. The heavy and light chain plasmids were transiently expressed in B11 CHO cells by cotransfection  
15 of the two plasmids using Transfectam (Promega, Southampton, UK). Culture supernatants were assayed for human IgG by ELISA, and tested for CD38-binding activity by FACS analysis using the CD38-positive B-cell line Wien 133.

20

Although the culture supernatants contained significant amounts of human IgG, no anti-CD38 activity could be detected by FACS, even when supernatants were concentrated 10-fold. This result suggests that simple  
25 grafting of the CDRs from AT13/5 onto the Campath 1H and REI human frameworks is insufficient to transfer the antibody specificity. A series of framework changes were therefore undertaken in order to restore CD38-binding activity.

30

(f) Framework changes

Since most of the framework residues previously shown to be important in restoring antigen binding are in the  
35 heavy chain variable region, it was decided to focus on



this part of the antibody. Additional cotransfection of the humanised light chain with a chimaeric heavy chain construct (mouse heavy variable region fused to human C<sub>H</sub>), produced active antibody (hereafter termed hybrid  
5 antibody) that bound CD38 with an affinity comparable to that of the original mouse antibody. The region with the lowest homology between the human frameworks used and the original mouse sequence is also close to some residues of known importance. This region, just downstream of the  
10 CDR3 sequence was chosen for mutagenesis.

Heavy chain residues 67 to 71 inclusive and 73 were grafted from the mouse antibody onto the humanised heavy chain using recombinant PCR. The primers used were as  
15 follows:

A<sub>H</sub>: sequence as above

I<sub>H</sub>: 5'GTTGTCCTTGGTGATGTTTCAGTCTGGACATGAAAGCTGC3'

J<sub>H</sub>: 5'CTGAACATCACCAAGGACAACAGCAAGAACCAGTTCAGC3'

20 H<sub>H</sub>: sequence as above.

Two initial PCRs were performed using 10ng of version 1 humanised heavy chain template with the primer pairs: A<sub>H</sub> and I<sub>H</sub> and J<sub>H</sub> and H<sub>H</sub>. The products of these reactions,  
25 AI<sub>H</sub> and JH<sub>H</sub> respectively, were gel-purified and half of the recovered DNA used in a second round of PCR with primers A<sub>H</sub> and H<sub>H</sub> to generate version 2 of the humanised heavy chain variable region. This was cloned, sequenced, transferred to the expression system, and then  
30 transiently co-expressed with the humanised light chain construct as above. Once again, culture supernatant from transfected CHO cells produced human IgG as determined by ELISA, but no CD38-binding activity could be detected by FACS analysis.

A further round of mutations based on both version 1 and version 2 of the humanised heavy chain were then produced by a method identical to that described above. A total of six version 3 heavy chains were produced in which the following heavy chain framework residues were grafted from the mouse sequence onto one or other humanised sequence:

	Antibody	Template for mutagenesis	Grafted residues	Primers used
10	h3J	version 1	28,29	K <sub>H</sub> , L <sub>H</sub>
	h3K	version 2	28,29	K <sub>H</sub> , L <sub>H</sub>
	h3L	version 1	76	M <sub>H</sub> , O <sub>H</sub>
	h3M	version 2	76	N <sub>H</sub> , O <sub>H</sub>
15	h3N	version 1	28,29,76	K <sub>H</sub> , L <sub>H</sub> , M <sub>H</sub> , O <sub>H</sub>
	h3O	version 2	28,29,76	K <sub>H</sub> , L <sub>H</sub> , N <sub>H</sub> , O <sub>H</sub>

Additionally, all constructions used primers A<sub>H</sub> and H<sub>H</sub>. The primer sequences used were:

20

A<sub>H</sub>: sequence as above

H<sub>H</sub>: sequence as above

K<sub>H</sub>: 5'ACTGGTTAACGAAAAGCCAGACACGGTGCAGGTCAG3'

L<sub>H</sub>: 5'GGCITTTTCGTAAACAGTTATGGTGTCCACTGGGTG3'

25

M<sub>H</sub>: 5'AAATTGCCGTTTTCGAAGTGTCTACCAGCATTGTCAC3'

N<sub>H</sub>: 5'AAATTGCCGTTTTCGAATTGTCCTTGGTGATGTTTCAG3'

O<sub>H</sub>: 5'TTCGAAACGGCAATTTAGCTTGAGACTCAGCAGC3'

Heavy chain constructs containing the expected sequence were transferred into mammalian expression vectors, and cotransfected with the humanised light chain construct into CHO cells, as above. Tissue culture supernatants containing human IgG as determined by ELISA were assayed for CD38-binding activity by FACS. Constructs h3K and h3O showed antigen-binding in this assay though with less

activity than the hybrid antibody (see Fig. 7).

(g) Method for changing framework residues at positions 29 and 78

5

In order to establish why h30 showed less activity than the hybrid antibody further sequences analysis suggested potential problems with positions 29 and 78 in the heavy chain.

10

Having identified mutations to be made in the heavy chain framework regions, these can be produced by a variety of standard methods: examples being site-directed mutagenesis, recombinant PCR and gene synthesis using oligonucleotides. In the case of the anti-CD38 heavy chain VH, recombinant PCR was used to introduce murine residues at positions 28-29 and 78 sequentially.

15

A human anti-CD38 heavy chain VH already incorporating murine residues at positions 27, 30, 67, 68, 69, 70, 71, 73 and 94 (Version 2 as described in (f) above) was used as template for the first round of mutagenesis. This was amplified with the following PCR primers in two separate reactions:

25

Primer A: 5'GATCAAGCTTTACAGTTACTCAGCACAG3'

Primer B: 5'ACTGGTTAACGAAAAGCCAGACACGGTGCAGGTCAG3'

Primer C: 5'GGCTTTTCGTTAACCAGTTATGGTGTCCACTGGGTG3'

Primer D: 5'TAGAGTCCTGAGGGAATTCGGACAGCCGGAAGGTG3'

30

In primers B and C, the triplets encoding the murine residues at positions 28 and 29 are underlined. In the first reaction, the template was amplified with primers A and B. In the second reaction, the template was amplified with primers C and D. The products of the two reactions were purified, mixed, and amplified with primers A and D. The reaction product was purified,

35

cleaved with Hind III and SpeI, and the 450 base-pair fragment encoding the VH cloned into a variant of pUC18 containing a human  $\gamma 1$  cDNA cassette (Sime et al, 1993; J. Immunol, 151:2296). Clones were sequenced to ensure  
5 correct introduction of the murine residues at positions 28 and 29.

A clone incorporating these changes was then used as template for a second round of recombinant PCR  
10 mutagenesis to introduce the murine residue at position 78. A procedure identical to that described above was followed, except that primers B and C were replaced by primers E and F respectively, which contain a triplet (underlined) that incorporates the murine residue at  
15 position 78.

Primer E: 5'AACCAGGTGAGCTTAAGACTCAGCAGCGTGACA3'

Primer F: 5'TCTTAAGCTCACCTGGTTCTTGCTGTTGTCCTT3'

20 The resulting heavy chain (see Fig. 4) when co-expressed with the humanised light chain (see Fig. 3) produces humanised anti-CD38,h3S.

(h) Eukaryotic expression of functional humanised  
25 antibody

To creat clonal cell lines for further characterisation, plasmids encoding the humanised h3S heavy chain and the chimaeric heavy chain were separately co-transfected with  
30 the humanised light chain into B11 CHO cells.

### Example 2

### Biological activity

## (a) CD38 Binding Studies

(i) Effect of various heavy chain framework substitutions on relative binding affinity of anti-CD38 antibodies.

5

Binding was assessed by FACS staining of CD38 positive cells.

Heavy chains incorporating one or more of mouse framework residues were created as described above and combined with the humanised light chain to make antibodies which were assayed for binding to CD38, with the following results.

15	Construct	66-73	28/29	78	Binding
	h1	-	-	-	-
	h2	+	-	-	-
	h3J	-	+	-	-
	h3K	+	+	-	+
20	h3S	+	+	+	++

In this table, + denotes that the murine framework residue is incorporated into the humanised antibody at the indicated position, - denotes that the human residue remains.

25

Discussion

According to computer modelling studies the change of the 66-73 region back to mouse framework causes the humanised CDRH2 to adopt a similar conformation to that of the mouse antibody. However, as the construct h2 shows, this is insufficient to obtain binding. The model also suggests that in the mouse anti-CD38 antibody, positions 29 and 78 are occupied by small residues, whose side-

35

chains pack neatly together allowing CDRH1 to adopt the correct configuration for antigen binding. In the humanised constructs h1 and h2, the side chains are unable to pack together in this fashion, being much larger, and so distort CDRH1, preventing antigen binding. This aspect of the model is illustrated in Figures 5 and 6 (attached). Figure 5 shows the configuration of CDRH1 (dark tubes) in the murine anti-CD38. In Figure 6 showing the same region in a humanised construct with human residues at positions 29 and 78, the extra bulk of these side chains has clearly resulted in a distortion of the CDRH1 conformation.

Partial relief of this effect can be obtained by using the murine residue at position 29 and the human residue at position 78, though the resulting antibody shows markedly reduced function. Use of murine residues at both positions 29 and 78 restores activity, as evidenced by the data for the h3S construct.

(ii) Anti-CD38 heavy chain variable regions were fused to human  $\gamma 1$  constant region and coexpressed in CHO cells with humanised anti-CD38 light chain. CD38-binding activity is expressed normalised to the signal obtained using a saturating dose of hybrid antibody (mouse VH) in the same experiment.

Results are shown in Figure 7 where:

- ◆ Humanised antibody with murine residues at 28,29 and 78
- ▲ Humanised antibody with murine residues at 28,29 and 76

● Humanised antibody with murine residues at 28,29

■ Hybrid antibody

5 In addition to the above substitutions, all humanised heavy chains contained murine framework residues at positions 27, 30, 67, 68, 69, 70, 71, 73 and 94. These alone are insufficient to obtain detectable binding by FACS.

10

These results demonstrate the critical importance of the small residues at positions 29 and/or 78 in obtaining full humanised heavy chain activity. They also demonstrate the specific nature of the interaction, in that a murine residue at position 76 close to position 78 was unable to restore activity.

15

(b) Effect of various heavy chain framework substitutions on antibody-dependent cellular cytotoxicity mediated by CD38 antibodies.

20

Antibody-dependent cellular cytotoxicity is normally assessed by one of several label-release techniques, well-known in the literature. In one such assay,  $10^4$  target cells (Wien 133) were labelled with europium and then exposed to freshly prepared human peripheral blood lymphocytes in the presence of antibody as an effector:target ratio of 50:1. Lysis was estimated by detecting release of europium after 4 hours, and quantitated by reference to control reactions without antibody or peripheral blood lymphocytes or with detergent such as Triton-X100.

25

The effect of framework substitutions on the lytic potential of humanised anti-CD38 monoclonals was examined

30

35

in label-release assay. Wien 133 target cells were loaded with label (either  $^{51}\text{Cr}$  or Eu) and then exposed to freshly prepared human peripheral blood mononuclear cells in the presence of varying amounts of anti-CD38 antibody. Cytotoxicity is expressed as the proportion of total releasable label liberated by antibody treatment.

Results are shown in Figure 10 where:

10

- ▲ Humanised antibody with murine residues at 28,29 and 78
- Humanised antibody with murine residues at 28,29 and 76
- 15 ● Hybrid antibody

These results show that the combination of framework changes at positions 29 and 78 confer full activity on the humanised heavy chain for cytotoxic function. Although incorporation of a small murine residue at position 29 results in some binding activity (Figure 7), this is insufficient to achieve full effector function.

20



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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(ii) TITLE OF INVENTION: ANTIBODIES

(iii) NUMBER OF SEQUENCES: 46

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

40

- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EP0)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..453

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGT CGA CTG GCT GTG TTA GCG CTG CTC TTC TGC CTG GTG ACA TTC CCA	48
Gly Arg Leu Ala Val Leu Ala Leu Leu Phe Cys Leu Val Thr Phe Pro	
1 5 10 15	
AGC TGT GTC CTG TCC CAG GTG CAG CTG AAG CAG TCA GGA CCT GGC CTA	96
Ser Cys Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu	
20 25 30	
GTG CAC CCC TCA CAG AGC CTG TCC ATA ACC TGC ACA GTC TCT GGT TTC	144
Val His Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe	
35 40 45	
TCA TTA ACT AGT TAT GGT GTC CAC TGG GTT CGC CAG TCT CCA GGA AAG	192

41

Ser	Leu	Thr	Ser	Tyr	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	
50						55						60				
GGT	CTG	GAG	TGG	CTG	GGA	GTG	ATG	TGG	AGA	GGT	GGA	AGC	ACA	GAC	TAC	240
Gly	Leu	Glu	Trp	Leu	Gly	Val	Met	Trp	Arg	Gly	Gly	Ser	Thr	Asp	Tyr	
65					70					75					80	
AAT	GCA	GCT	TTC	ATG	TCC	AGA	CTG	AAC	ATC	ACC	AAG	GAC	AAC	TCC	AAG	288
Asn	Ala	Ala	Phe	Met	Ser	Arg	Leu	Asn	Ile	Thr	Lys	Asp	Asn	Ser	Lys	
				85					90					95		
CGC	CAG	GTT	TTC	TTT	AAA	ATG	AAC	AGT	CTA	CAA	GCT	GAT	GAC	ACT	GCC	336
Arg	Gln	Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Ala	Asp	Asp	Thr	Ala	
			100					105						110		
ATA	TAC	TAC	TGT	GCC	AAA	TCG	ATG	ATT	ACG	ACG	GGC	TTT	GTT	ATG	GAC	384
Ile	Tyr	Tyr	Cys	Ala	Lys	Ser	Met	Ile	Thr	Thr	Gly	Phe	Val	Met	Asp	
			115					120						125		
TCC	TGG	GGT	CAA	GGA	ACC	TCA	GTC	ACC	GTC	TCC	TCA	GCC	AAA	ACG	ACA	432
Ser	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	
			130					135						140		
CCC	CCA	TCT	GTC	TAT	CCA	CTG	G									454
Pro	Pro	Ser	Val	Tyr	Pro	Leu										
145						150										

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

42

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gly Arg Leu Ala Val Leu Ala Leu Leu Phe Cys Leu Val Thr Phe Pro  
1 5 10 15

Ser Cys Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu  
20 25 30

Val His Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe  
35 40 45

Ser Leu Thr Ser Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys  
50 55 60

Gly Leu Glu Trp Leu Gly Val Met Trp Arg Gly Gly Ser Thr Asp Tyr  
65 70 75 80

Asn Ala Ala Phe Met Ser Arg Leu Asn Ile Thr Lys Asp Asn Ser Lys  
85 90 95

Arg Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala  
100 105 110

Ile Tyr Tyr Cys Ala Lys Ser Met Ile Thr Thr Gly Phe Val Met Asp  
115 120 125

Ser Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr  
130 135 140

Pro Pro Ser Val Tyr Pro Leu  
145 150

(2) INFORMATION FOR SEQ ID NO: 3:

43

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iv) ANTI-SENSE: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCAGCTGACC GACACAATCG CGACGAGAAG ACGGACCACT GTAAGGGTTC GACACAGGAC	60
AGGGTCCACG TCGACTTCGT CAGTCCTGGA CCGGATCACG TGGGGAGTGT CTCGGACAGG	120
TATTGGACGT GTCAGAGACC AAAGAGTAAT TGATCAATAC CACAGGTGAC CCAAGCGGTC	180
AGAGGTCCTT TCCCAGACCT CACCGACCCT CACTACACCT CTCCACCTTC GTGTCTGATG	240
TTACGTCGAA AGTACAGGTC TGACTIONTAG TGGTTCCTGT TGAGGTTCGC GGTCCAAAAG	300
AAATTTTACT TGTCAGATGT TCGACTACTG TGACGGTATA TGATGACACG GTTTAGCTAC	360
TAATGCTGCC CGAAACAATA CCTGAGGACC CCAGTTCCTT GGAGTCAGTG GCAGAGGAGT	420
CGGTTTTGCT GTGGGGGTAG ACAGATAGGT GACC	454

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid

44

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC TTT TCT GTT TCT CTA GGA	48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Phe Ser Val Ser Leu Gly	
155 160 165	
GAC AGA GTC ACC ATT ACT TGC AAG GCA AGT GAG GAC ATA TAT AAT CGG	96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg	
170 175 180	
TTA ACC TGG TAT CAG CAG AAA CCA GGA AAT GCT CCT AGG CTC TTA ATA	144
Leu Thr Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu Leu Ile	
185 190 195	
TCT GGT GCA ACC AGT TTG GAA ACT GGG GTT CCT TCA AGA TTC AGT GGC	192
Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly	
200 205 210 215	
AGT GGA TCT GGA AAG GAT TAC ACT CTC AGC ATT ACC AGT CTT CAG ACT	240
Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr	
220 225 230	
GAA GAT GTT GCT ACC TAT TAC TGT CAA CAG TAT TGG AGT AAT CCG TAC	288
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Asn Pro Tyr	
235 240 245	

45

ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AGA CGG GCT GAT GCT GCA 336  
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala  
 250 255 260

CCA ACT GTA TCC ATC TTC CCA CCA TCC A 364  
 Pro Thr Val Ser Ile Phe Pro Pro Ser  
 265 270

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Phe Ser Val Ser Leu Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg  
 20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu Leu Ile  
 35 40 45

Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr  
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Asn Pro Tyr

46  
85 90 95  
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala  
100 105 110  
Pro Thr Val Ser Ile Phe Pro Pro Ser  
115 120

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGTAAGTCG ACTGGGTCAG AGGTAGGAGG AAAAGACAAA GAGATCCTCT GTCTCAGTGG	60
TAATGAACGT TCGTTCACT CCTGTATATA TTAGCCAATT GGACCATAGT CGTCTTTGGT	120
CCTTTACGAG GATCCGAGAA TTATAGACCA CGTTGGTCAA ACCTTTGACC CCAAGGAAGT	180
TCTAAGTCAC CGTCACCTAG ACCTTTCCTA ATGTGAGAGT CGTAATGGTC AGAAGTCTGA	240
CTTCTACAAC GATGGATAAT GACAGTTGTC ATAACCTCAT TAGGCATGTG CAAGCCTCCC	300
CCCTGGTTCG ACCTTTATTC TGCCCGACTA CGACGTGGTT GACATAGGTA GAAGGGTGGT	360



47

AGGT

364

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:3..737

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AA GCT TCT CTA CAG TTA CTG AGC ACA CAG GAC CTC ACC ATG GGA TGG	47
Ala Ser Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Gly Trp	
125 130 135	
AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC	95
Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val His Ser	
140 145 150	
GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT	143
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly	
155 160 165	
GAC AGA GTG ACC ATC ACC TGT AAG GCA AGT GAG GAC ATA TAT AAT CGG	191
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg	
170 175 180	

48

TTA ACC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC 239  
 Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 185 190 195 200

TCT GGT GCA ACC AGT TTG GAA ACT GGT GTG CCA AGC AGA TTC AGC GGT 287  
 Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly  
 205 210 215

AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA 335  
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro  
 220 225 230

GAG GAC ATC GCC ACC TAC TAC TGC CAA CAG TAT TGG AGT AAT CCG TAC 383  
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Asn Pro Tyr  
 235 240 245

ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA 431  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 250 255 260

CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA 479  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 265 270 275 280

ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG GCC 527  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 285 290 295

AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG 575  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 300 305 310

GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC 623  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 315 320 325

49

AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC 671  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 330 335 340

GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC 719  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 345 350 355 360

TTC AAC AGG GGA GAG TGT TAGAAGCTT 746  
 Phe Asn Arg Gly Glu Cys  
 365

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Ser Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Gly Trp Ser  
 1 5 10 15

Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val His Ser Asp  
 20 25 30

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp  
 35 40 45

Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu  
 50 55 60

50

Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Ser  
65 70 75 80

Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser  
85 90 95

Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
100 105 110

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Asn Pro Tyr Thr  
115 120 125

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro  
130 135 140

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
145 150 155 160

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
165 170 175

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
180 185 190

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser  
195 200 205

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
210 215 220

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
225 230 235 240

Asn Arg Gly Glu Cys  
245

**(2) INFORMATION FOR SEQ ID NO: 9:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 746 base pairs
- (B) TYPE:** nucleic acid
- (C) STRANDEDNESS:** double
- (D) TOPOLOGY:** linear

**(iv) ANTI-SENSE: YES****(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:**

TTCGAAGAGA TGTCAATGAC TCGTGTGTCC TGGAGTGGTA CCCTACCTCG ACATAGTAGG	60
AGAAGAACCA TCGTTGTCGA TGTCCACAGG TGAGGCTGTA GGTCTACTGG GTCTCGGGTT	120
CGTCGGACTC GCGGTCGCAC CCACTGTCTC ACTGGTAGTG GACATTCCGT TCACTCCTGT	180
ATATATTAGC CAATTGGACC ATGGTCGTCT TCGGTCCATT CCGAGGTTTC GACGACTAGA	240
GACCACGTTG GTCAAACCTT TGACCACACG GTTCGTCTAA GTCGCCATCG CCATCGCCAT	300
GGCTGAAGTG GAAGTGGTAG TCGTCGGAGG TCGGTCTCCT GTAGCGGTGG ATGATGACGG	360
TTGTCATAAC CTCATTAGGC ATGTGCAAGC CGGTTCCCTG GTTCCACCTT TAGTTTGCTT	420
GACACCGACG TGGTAGACAG AAGTAGAAGG GCGGTAGACT ACTCGTCAAC TTTAGACCTT	480
GACGGAGACA ACACACGGAC GACTTATTGA AGATAGGGTC TCTCCGTTT CATGTCACCT	540
TCCACCTATT GCGGGAGGTT AGCCCATTTGA GGGTCCTCTC ACAGTGTCTC GTCCTGTCGT	600

52

TCCTGTCGTG GATGTCGGAG TCGTCGTGGG ACTGCGACTC GTTTCGTCTG ATGCTCTTTG 660  
 TGTTTCAGAT GCGGACGCTT CAGTGGGTAG TCCCGGACTC GAGCGGGCAG TGTTTCTCGA 720  
 AGTTGTCCCC TCTCACAATC TTCGAA 746

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:3..14

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:18..434

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AA GCT TTA CAG TTA CNC AGC ACA CAG GAC CTC ACC ATG GGA TGG AGC	47
Ala Leu Gln Leu Ser Thr Gln Asp Leu Thr Met Gly Trp Ser	
1 5 10	
TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG	95
Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val His Ser Gln	
15 20 25	

53

GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA CCT AGC CAG ACC	143
Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr	
30 35 40	
CTG AGC CTG ACC TGC ACC GTG TCT GGC TTT TCG TTA ACC AGT TAT GGT	191
Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly	
45 50 55	
GTC CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT GAG TGG ATT GGA	239
Val His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly	
60 65 70	
GTG ATG TGG AGA GGT GGA AGC ACA GAC TAC AAT GCA GCT TTC ATG TCC	287
Val Met Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met Ser	
75 80 85 90	
AGA CTG AAC ATC ACC AAG GAC AAC AGC AAG AAC CAG GTG AGC TTA AGA	335
Arg Leu Asn Ile Thr Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Arg	
95 100 105	
CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC TAT TAT TGT GCA AAA	383
Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys	
110 115 120	
TCC ATG ATA ACG ACC GGC TTC GTG ATG GAC TCC TGG GGT CAA GGC TCA	431
Ser Met Ile Thr Thr Gly Phe Val Met Asp Ser Trp Gly Gln Gly Ser	
125 130 135	
CTA GT	436
Leu	

(2) INFORMATION FOR SEQ ID NO: 11:

54

**(i) SEQUENCE CHARACTERISTICS:****(A) LENGTH: 4 amino acids****(B) TYPE: amino acid****(D) TOPOLOGY: linear****(ii) MOLECULE TYPE: protein****(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:****Ala Leu Gln Leu****1****(2) INFORMATION FOR SEQ ID NO: 12:****(i) SEQUENCE CHARACTERISTICS:****(A) LENGTH: 139 amino acids****(B) TYPE: amino acid****(D) TOPOLOGY: linear****(ii) MOLECULE TYPE: protein****(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:**

**Ser Thr Gln Asp Leu Thr Met Gly Trp Ser Cys Ile Ile Leu Phe Leu**  
**1 5 10 15**

**Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu Gln Glu Ser**  
**20 25 30**

**Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr**  
**35 40 45**

**Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly Val His Trp Val Arg Gln**  
**50 55 60**

**Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Val Met Trp Arg Gly Gly**



55

65	70	75	80
Ser Thr Asp Tyr Asn Ala Ala Phe Met Ser Arg Leu Asn Ile Thr Lys			
	85	90	95
Asp Asn Ser Lys Asn Gln Val Ser Leu Arg Leu Ser Ser Val Thr Ala			
	100	105	110
Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ser Met Ile Thr Thr Gly			
	115	120	125
Phe Val Met Asp Ser Trp Gly Gln Gly Ser Leu			
	130	135	

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TTCGAAATGT CAATGNGTCG TGTGTCCTGG AGTGGTACCC TACCTCGACA TAGTAGGAGA	60
AGAACCATCG TTGTCGATGT CCACAGGTGA GGGTCCAGGT TGACGTCCTC TCGCCAGGTC	120
CAGAACACTC TGGATCGGTC TGGGACTCGG ACTGGACGTG GCACAGACCG AAAAGCAATT	180

56

GGTCAATACC ACAGGTGACC CACTCTGTCG GTGGACCTGC TCCAGAACTC ACCTAACCTC 240  
ACTACACCTC TCCACCTTCG TGTCTGATGT TACGTCGAAA GTACAGGTCT GACTTGTAGT 300  
GGTTCCTGTT GTCGTTCTTG GTCCACTCGA ATTCTGAGTC GTCGCACTGT CGGCGGCTGT 360  
GGCGCCAGAT AATAACACGT TTTAGGTACT ATTGCTGGCC GAAGCACTAC CTGAGGACCC 420  
CAGTTCCGAG TGATCA 436

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GACATTCAGC TGACCCAGTC TCCA 24

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA

34

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACTAGTCGAC CATCCTCCTT TTCTGTTTCT CTAGGAG

37

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

58

GATCAAGCTT CTCTACAGTT ACTGAGCACA

30

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CCGATTATAT ATGTCCTCAC TTGCCTTACA GGTGATGGTC AC

42

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AGTGAGGACA TATATAATCG GTTAACCTGG TACCAGCAGA AG

42

## (2) INFORMATION FOR SEQ ID NO: 20:

59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AGTTTCCAAA CTGGTTGCAC CAGAGATCAG CAGCTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGTGCAACCA GTTTGGAAAC TGGTGTGCCA AGCAGA

36

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid

60

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTACGGATTA CTCCAATACT GTTGGCAGTA GTAGGTGGC

39

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CAGTATTGGA GTAATCCGTA CACGTTCGGC CAAGGGACC

39

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GATCAAGCTT CTAACACTCT CCCCTGTTGA

30

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GATCAAGCTT TACAGTTACT CAGCACACAG

30

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTGGACACCA TAACTGGTGA AGGTGAAGCC

30

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AGTTATGGTG TCCACTGGGT GAGACAGCCA

30

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTGTAGTCTG TGCTTCCACC TCTCCACATC ACTCCAATCC ACTCAAG

47



63

**(2) INFORMATION FOR SEQ ID NO: 29:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 51 base pairs**
- (B) TYPE: nucleic acid**
- (C) STRANDEDNESS: single**
- (D) TOPOLOGY: linear**

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:**

GGAGTCCATC ACGAAGCCGG TCGTTATCAT GGATTTTGCA CAATAATAGA C

51

**(2) INFORMATION FOR SEQ ID NO: 30:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 72 base pairs**
- (B) TYPE: nucleic acid**
- (C) STRANDEDNESS: single**
- (D) TOPOLOGY: linear**

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:**

AAATCCATGA TAACGACCGG CTTCGTGATG GACTCCTGGG GTCAAGGCTC ACTAGTCACA

60

GTCTCCTCAG CC

72

**(2) INFORMATION FOR SEQ ID NO: 31:**

64

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TAGAGTCCTG AGGGAATTCG GACAGCCGGG AAGGTG

36

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTTGTCCTTG GTGATGTTCA GTCTGGACAT GAAAGCTGC

39

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid

65

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGAACATCA CCAAGGACAA CAGCAAGAAC CAGTTCAGC

39

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

ACTGGTTAAC GAAAAGCCAG ACACGGTGCA GGTCAG

36

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGCTTTTCGT TAACCAGTTA TGGTGTCAC TGGGTG

36

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

AAATTGCCGT TTCGAAGTGT CTACCAGCAT TGTCAC

36

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AAATTGCCGT TTCGAATTGT CCTTGGTGAT GTTCAG

36

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TTCGAAACGG CAATTTAGCT TGAGACTCAG CAGC

34

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAAGCACAGA CTACAATGCA GCTTTCATGT CCAGAGTGAC AATGCTG

47

68

**(2) INFORMATION FOR SEQ ID NO: 40:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 28 base pairs**
- (B) TYPE: nucleic acid**
- (C) STRANDEDNESS: single**
- (D) TOPOLOGY: linear**

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:**

**GATCAAGCTT TACAGTTACT CAGCACAG**

**28**

**(2) INFORMATION FOR SEQ ID NO: 41:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 36 base pairs**
- (B) TYPE: nucleic acid**
- (C) STRANDEDNESS: single**
- (D) TOPOLOGY: linear**

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:**

**ACTGGTTAAC GAAAAGCCAG ACACGGTGCA GGTCAG**

**36**

**(2) INFORMATION FOR SEQ ID NO: 42:**

**(i) SEQUENCE CHARACTERISTICS:**

69

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GGCTTTTCGT TAACCAGTTA TGGTGCCAC TGGGTG

36

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

TAGAGTCCTG AGGGAATTCG GACAGCCGGG AAGGTG

36

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

70

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AACCAGGTGA GCTTAAGACT CAGCAGCGTG ACA

33

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TCTTAAGCTC ACCTGGTTCT TGCTGTTGTC CTT

33

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Ser Tyr Gly Val His

1

5

## CLAIMS:

1. A monoclonal antibody having donor CDRs of foreign origin and a recipient framework region having a sequence  
5 of human or primate origin, wherein the original amino acid residue in position 29 or 78 of the sequence of the recipient framework region of the heavy chain is replaced by a replacement amino acid residue that is the same or similar to that in the corresponding position of the  
10 sequence of the corresponding framework region of the heavy chain of the antibody from which the CDRs are derived.
2. A monoclonal antibody according to claim 1, wherein  
15 the original amino acid residues in both positions 29 and 78 of the sequence of the recipient framework region of the heavy chain are replaced by replacement amino acids that are the same or similar to the amino acids in the corresponding positions of the corresponding framework  
20 region of the antibody from which the CDRs are derived.
3. A monoclonal antibody according to claim 1 or 2, wherein one or both of the original amino acid residues of the recipient framework region are replaced by a  
25 replacement amino acid residues of similar size, hydrophobicity and charge to the amino acids in the corresponding positions of the corresponding framework region of the antibody from which the CDRs are derived.
- 30 4. A monoclonal antibody according to any of the preceding claims, wherein the original amino acid residues of the recipient framework region are the same or different and are tyrosine, histidine, tryptophan or 2-phenyl-alanine.

5. A monoclonal antibody according to claim 4, wherein the replacement amino acid residues are the same or different and are selected from glycine, alanine, valine, serine or leucine.
- 5 6. A monoclonal antibody according to any of the preceding claims wherein the recipient framework region is from a heavy chain selected from LES-C, T52, Ab44, HIGI and NEW.
- 10 7. A monoclonal antibody according to any of the preceding claims, wherein the CDRs are of rat, mouse rabbit, or hamster origin.
- 15 8. A monoclonal antibody according to any of the preceding claims, wherein the heavy chain of the antibody from which the CDRs are derived is a murine heavy chain in Kabat groups IB and IIC.
- 20 9. A monoclonal antibody according to any of the preceding claims wherein the antibody binds to CD38.
10. A monoclonal antibody according to claim 9 having a nucleotide sequence as shown in figures 3, 3a and 4.
- 25 11. A monoclonal antibody according to any of the preceding claims, wherein the donor CDR is CDRHI.
12. A monoclonal antibody according to claim 11, wherein CDRHI has a sequence of SYGVH.
- 30 13. A method of producing an antibody according to any of the above claims comprising the steps of:
- 35 (i) obtaining the sequence of a donor heavy chain;

- (ii) selecting a recipient human or primate framework by best-fit homology method;
- (iii) replacing the amino acid residue in position 29 or 78 of the sequence of the recipient framework region of the heavy chain by an amino acid that is the same or similar to that in the corresponding position of the sequence of the corresponding framework region of the antibody from which the CDRs are derived;
- (iv) grafting donor CDRs into the recipient human framework.
14. Use of an antibody according to any of the preceding claims for the treatment of cancer and autoimmune diseases.
15. Use of an antibody according to claim 9 or 10 for treatment of multiple myeloma, lymphoma and autoimmune diseases such as rheumatoid arthritis.
16. Use of an antibody according to any of claims 1 to 12 for the manufacture of a medicament for the treatment of cancer or an autoimmune disease.
17. Use of an antibody according to any of claims 1 to 12 for the manufacture of a medicament for the treatment of multiple myeloma, lymphoma, or rheumatoid arthritis.
18. A pharmaceutical composition comprising an antibody according to any of claims 1 to 12 and a physiologically acceptable diluent or carrier.

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GGTCGACTGGCTGTGTTAGCGCTGCTCTTCTGCCTGGTgACATTCCCAAGCTGTGTCCTG
1  -----+-----+-----+-----+-----+ 60
CCAGCTGACCGACACAATCGCGACGAGAAGACGGACCacTGTAAAGGGTTCGACACAGGAC

a    G R L A V L A L L F C L V T F P S C V L  -

TCCCAGGTGCAGCTGAAGCAGTCAGgaCCTGGCCTAGTGCACCCCTCACAGAGCCTGTCC
61  -----+-----+-----+-----+-----+ 120
AGGGTCCACGTGCGACTTCGTTCAGTCctGGACCGGATCACGTGGGGAGTGTCTCGGACAGG

a    S Q V Q L K Q S G P G L V H P S Q S L S  -

ATAACCTGCACAGTCTCTGGTTTCTCATTAACTAGTTATGGTGTCCACTGGGTTCGCCAG
121 -----+-----+-----+-----+-----+ 180
TATTGGACGTGTTCAGAGACCAAAGAGTAATTGATCAATACCACAGGTGACCCAAGCGGTC

a    I T C T V S G F S L T S Y G V H W V R Q  -

TCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATGTGGAGAGGTGGAAGCACAGACTAC
181 -----+-----+-----+-----+-----+ 240
AGAGGTCCCTTTCCCAGACCTCACCGACCCCTCACTACACCTCTCCACCTTCGTGTCTGATG

a    S P G K G L E W L G V M W R G G S T D Y  -

aATgCAGCTTTTCatGTCCAGACTGAACatcACCAAGGACAACCTCCAAGCGCCAGGTTTTTC
241 -----+-----+-----+-----+-----+ 300
tTAcGTCGAAAGTACAGGTCTGACTTGTgTagTGGTTCCTGTTGAGGTTTCGCGGTCCAAAAG

a    N A A F M S R L N I T K D N S K R Q V F  -

TTTAAATGAACAGTCTACAAGCTGATGACACTGCCATATACTACTGTGCCAAATCGATG
301 -----+-----+-----+-----+-----+ 360
AAATTTTACTTGTTCAGATGTTTCGACTACTGTGACGGTATATGATGACACGGTTTtagCTAC

a    F K M N S L Q A D D T A I Y Y C A K S M  -

ATTACGACGGGCTTTGTTATGGACTCCTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
361 -----+-----+-----+-----+-----+ 420
TAATGCTGCCCCGAAACAATACCTGAGGACCCAGTTTCCTTGGAGTCAGTGGCAGAGGAGT

a    I T T G F V M D S W G Q G T S V T V S S  -

GCCAAAACGACACCCCCATCTGTCTATCCACTGG
421 -----+-----+-----+-----+ 454
CGGTTTTGCTGTGGGGGTAGACAGATAGGTGACC

a    A K T T P P S V Y P L  -

```

Fig. 1

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GACATTCAGCTGACCCAGTCTCCATCCTCCTTTTCTGTTTCTCTAGGAGACAGAGTCACC  
1 -----+-----+-----+-----+-----+-----+ 60  
CTGTAAGTCGACTGGGTCAGAGGTAGGAGGAAAAGACAAAGAGATCCTCTGTCTCAGTGG

a D I Q L T Q S P S S F S V S L G D R V T -

ATTACTTGCAAGGCAAGTGAGGACATATATAATCGGTAACTGGTATCAGCAGAAACCA  
61 -----+-----+-----+-----+-----+-----+ 120  
TAATGAACGTTCCGTTCACTCCTGTATATATTAGCCAATTGGACCATAGTCGTCTTTGGT

a I T C K A S E D I Y N R L T W Y Q Q K P -

GGAAATGCTCCTAGGCTCTTAATATCTGGTGCAACCAGTTTGGAACCTGGGGTTCCTTCA  
121 -----+-----+-----+-----+-----+-----+ 180  
CCTTTACGAGGATCCGAGAATTATAGACCACGTTGGTCAAACCTTTGACCCCAAGGAAGT

a G N A P R L L I S G A T S L E T G V P S -

AGATTCAGTGGCAGTGGATCTGGAAAGGATTACACTCTCAGCATTACCAGTCTTCAGACT  
181 -----+-----+-----+-----+-----+-----+ 240  
TCTAAGTCACCGTCACCTAGACCTTTCTAATGTGAGAGTCGTAATGGTCAGAAGTCTGA

a R F S G S G S G K D Y T L S I T S L Q T -

GAAGATGTTGCTACCTATTACTGTCAACAGTATTGGAGTAATCCGTACACGTTCCGGAGGG  
241 -----+-----+-----+-----+-----+-----+ 300  
CTTCTACAACGATGGATAATGACAGTTGTGCATAACCTCATTAGGCATGTGCAAGCCTCCC

a E D V A T Y Y C O O Y W S N P Y T F G G -

GGGACCAAGCTGGAAATAAGACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA  
301 -----+-----+-----+-----+-----+-----+ 360  
CCCTGGTTCGACCTTTATTCTGCCCGACTACGACGTGGTTGACATAGGTAGAAGGGTGGT

a G T K L E I R R A D A A P T V S I F P P -

TCCA  
361 ---- 364  
AGGT

a S -

Fig. 2

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```

AAGCTTCTCTACAGTTACTGAGCACACAGGACCTCACCATGGGATGGAGCTGTATCATCC
1 -----+-----+-----+-----+-----+-----+-----+ 60
TTCGAAGAGATGTCAATGACTCGTGTGTCTCTGGAGTGGTACCCTACCTCGACATAGTAGG

c      A S L Q L L S T Q D L T M G W S C I I L -

TCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCGACATCCAGATGACCCAGAGCCCAA
61 -----+-----+-----+-----+-----+-----+-----+ 120
AGAAGAACCATCGTTGTGCGATGTCCACAGGTGAGGCTGTAGGTCTACTGGGTCTCGGGTT

c      F L V A T A T G V H S D I Q M T Q S P S -

GCAGCCTGAGCGCCAGCGTGGGTGACAGAGTGACCATCACCTGTAAGGCAAGTGAGGACA
121 -----+-----+-----+-----+-----+-----+-----+ 180
CGTCGGACTCGCGGTGCGACCCACTGTCTCACTGGTAGTGACATTCCGTTCACTCCTGT

c      S L S A S V G D R V T I T C K A S E D I -

TATATAATCGGTTAACCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCT
181 -----+-----+-----+-----+-----+-----+-----+ 240
ATATATTAGCCAATTGGACCATGGTTCGTCTTCGGTCCATTCCGAGGTTTCGACGACTAGA

c      Y N R L T W Y Q Q K P G K A P K L L I S -

CTGGTGCAACCAGTTTGGAAACTGGTGTGCCAAGCAGATTTCAGCGGTAGCGGTAGCGGTA
241 -----+-----+-----+-----+-----+-----+-----+ 300
GACCACGTTGGTCAAACCTTTGACCACACGGTTCGTCTAAGTCGCCATCGCCATCGCCAT

c      G A T S L E T G V P S R F S G S G S G T -

CCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACATCGCCACCTACTACTGCC
301 -----+-----+-----+-----+-----+-----+-----+ 360
GGCTGAAGTGGAAGTGGTAGTCGTGCGAGGTGGTCTCCTGTAGCGGTGGATGATGACGG

c      D F T F T I S S L Q P E D I A T Y Y C Q -

AACAGTATTGGAGTAATCCGTACACGTTTCGGCCAAGGGACCAAGGTGGAATCAAACGAA
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTGTCATAACCTCATTAGGCATGTGCAAGCCGGTTCCTGTTCCACCTTTAGTTTGCTT

c      Q Y W S N P Y T F G Q G T K V E I K R T -

CTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAA
421 -----+-----+-----+-----+-----+-----+-----+ 480
GACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTT

c      V A A P S V F I F P P S D E Q L K S G T -

CTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA
481 -----+-----+-----+-----+-----+-----+-----+ 540
GACGGAGACAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCT

c      A S V V C L L N N F Y P R E A K V Q W K -

AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA
541 -----+-----+-----+-----+-----+-----+-----+ 600
TCCACCTATTGCGGGAGGTTAGCCCATTTAGAGGTCCTCTCACAGTGTCTCGTCCTGTCGT

c      V D N A L Q S G N S Q E S V T E Q D S K -

AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
601 -----+-----+-----+-----+-----+-----+-----+ 660
TCCTGTCGTGGATGTGCGAGTCGTGCTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTG

```

Fig. 3

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c            D S T Y S L S S T L T L S K A D Y E K H -  
             ACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT  
661 -----+-----+-----+-----+-----+-----+ 720  
             TGTTCAGATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTCGCGA  
c            K V Y A C E V T H Q G L S S P V T K S F -  
             TCAACAGGGGAGAGTGTTAGAAGCTT  
721 -----+-----+-----+-----+ 660  
             AGTTGTCCCCTCTCACAATCTTCGAA  
c            N R G E C \* K L -

*Fig. 3a*



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AAGCTTTACAGTTACXCAGCACACAGGACCTCACCATGGGATGGAGCTGTATCATCCTCT  
1 -----+-----+-----+-----+-----+ 60  
TTCGAAATGTCAATGXGTCGTGTGTCCTGGAGTGGTACCCTACCTCGACATAGTAGGAGA

c        A L Q L ? S T Q D L T M G W S C I I L F -

TCTTGGTAGCAACAGCTACAGGTGTCCACTCCCAGGTCCAAGTGCAGGAGAGCGGTCCAG  
61 -----+-----+-----+-----+-----+ 120  
AGAACCATCGTTGTGCGATGTCCACAGGTGAGGGTCCAGGTTGACGTCCTCTCGCCAGGTC

c        L V A T A T G V H S Q V Q L Q E S G P G -

GTCTTGTGAGACCTAGCCAGACCCTGAGCCTGACCTGCACCGTGTCTGGCTTTTCGTTAA  
121 -----+-----+-----+-----+-----+ 180  
CAGAACACTCTGGATCGGTCTGGGACTCGGACTGGACGTGGCACAGACCGAAAAGCAATT

c        L V R P S Q T L S L T C T V S G F S L T -

CCAGTTATGGTGTCCACTGGGTGAGACAGCCACCTGGACGAGGTCTTGAGTGGATTGGAG  
181 -----+-----+-----+-----+-----+ 240  
GGTCAATACCACAGGTGACCCACTCTGTGCGTGGACCTGCTCCAGAACTCACCTAACCTC

c        S Y G V H W V R Q P P G R G L E W I G Y -

TGATGTGGAGAGGTGGAAGCACAGACTACAATGCAGCTTTCATGTCCAGACTGAACATCA  
241 -----+-----+-----+-----+-----+ 300  
ACTACACCTCTCCACCTTCGTGTCTGATGTTACGTGCAAAGTACAGGTCTGACTTGTAGT

c        M W R G G S T D Y N A A F M S R L N I T -

CCAAGGACAACAGCAAGAACCAGGTGAGCTTAAGACTCAGCAGCGTGACAGCCGCCGACA  
301 -----+-----+-----+-----+-----+ 360  
GGTTCCTGTTGTCGTTCTTGGTCCACTCGAATTCTGAGTCGTCGACTGTGCGCGGCTGT

c        K D N S K N Q V S L R L S S V T A A D T -

CCGCGGTCTATTATTGTGCAAAATCCATGATAACGACCGGCTTCGTGATGGACTCCTGGG  
361 -----+-----+-----+-----+-----+ 420  
GGCGCCAGATAATAACACGTTTTAGGTACTATTGCTGGCCGAAGCACTACCTGAGGACCC

c        A V Y Y C A K S M I T T G F V M D S W G -

GTCAAGGCTCACTAGT  
421 -----+----- 436  
CAGTTCCGAGTGATCA

c        Q G S L -

Fig. 4

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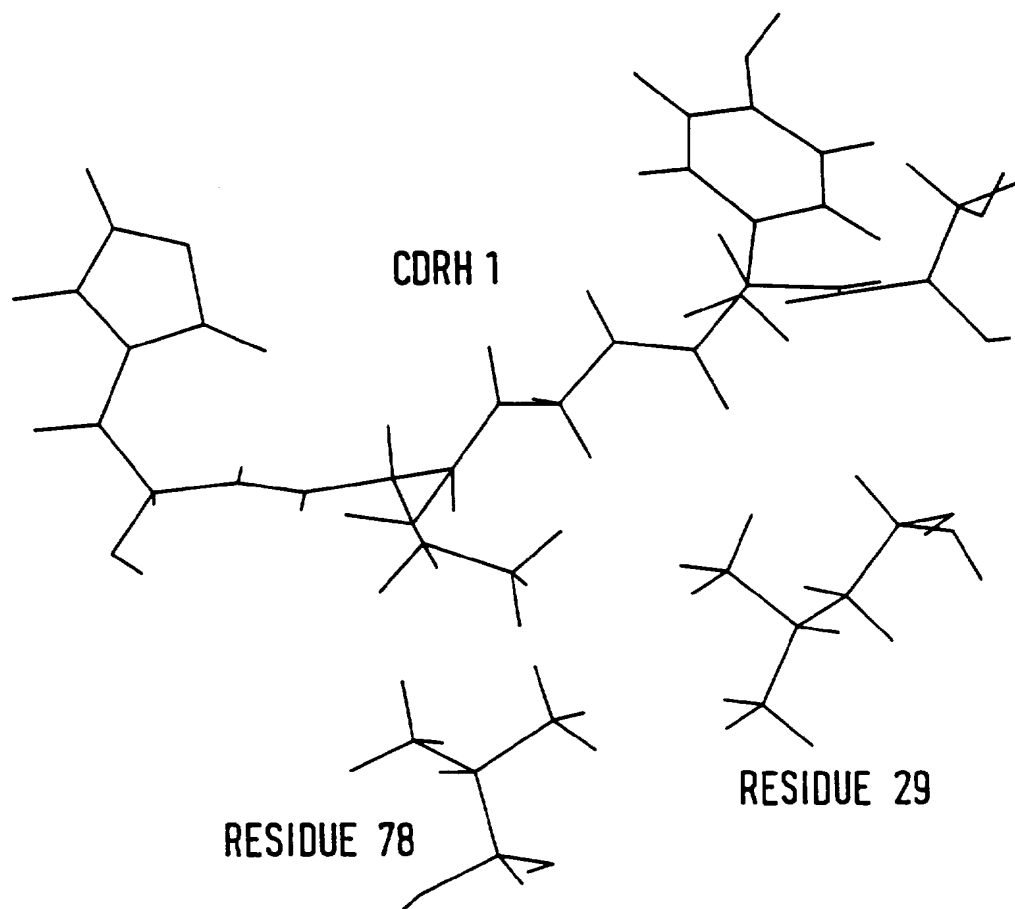
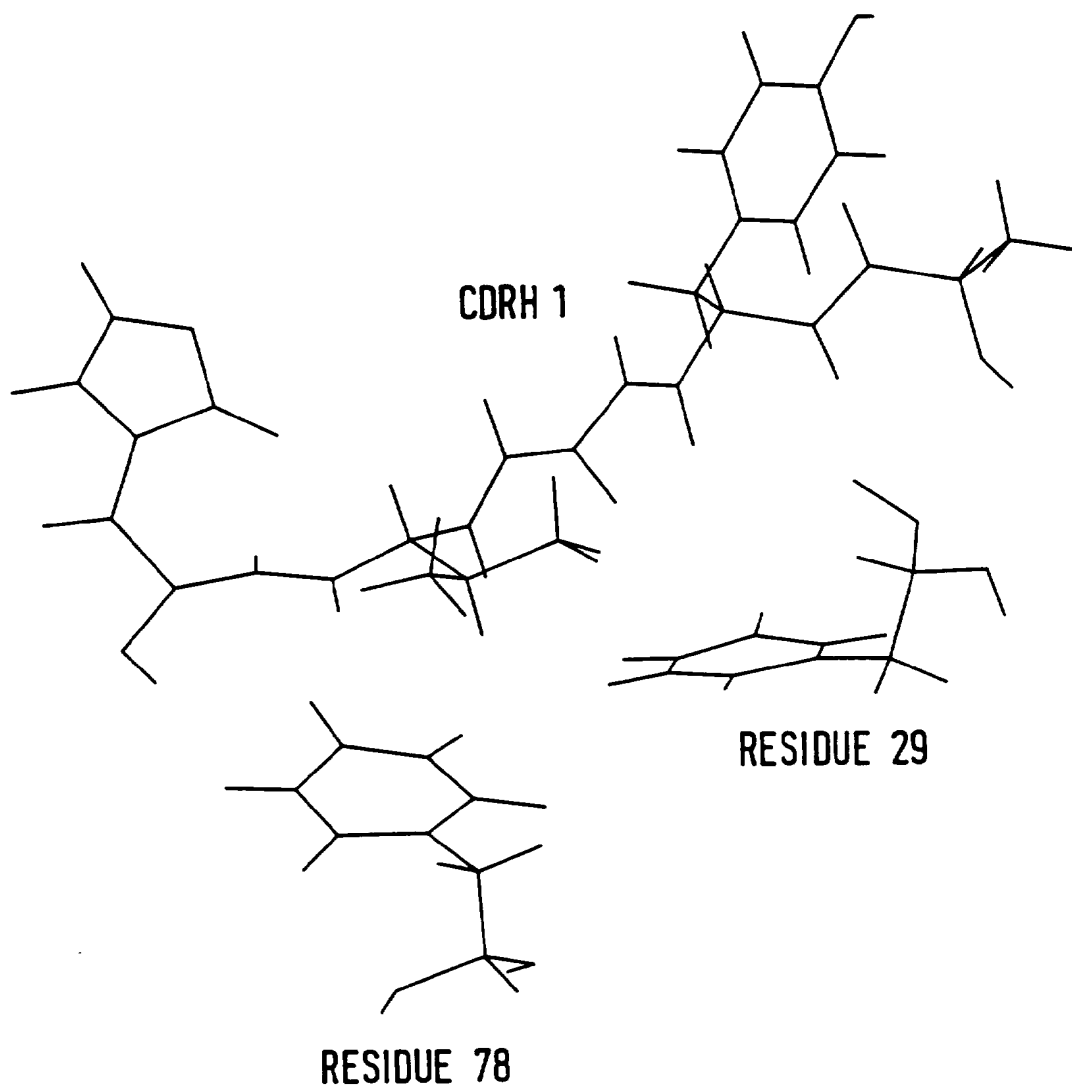


Fig. 5

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*Fig. 6*

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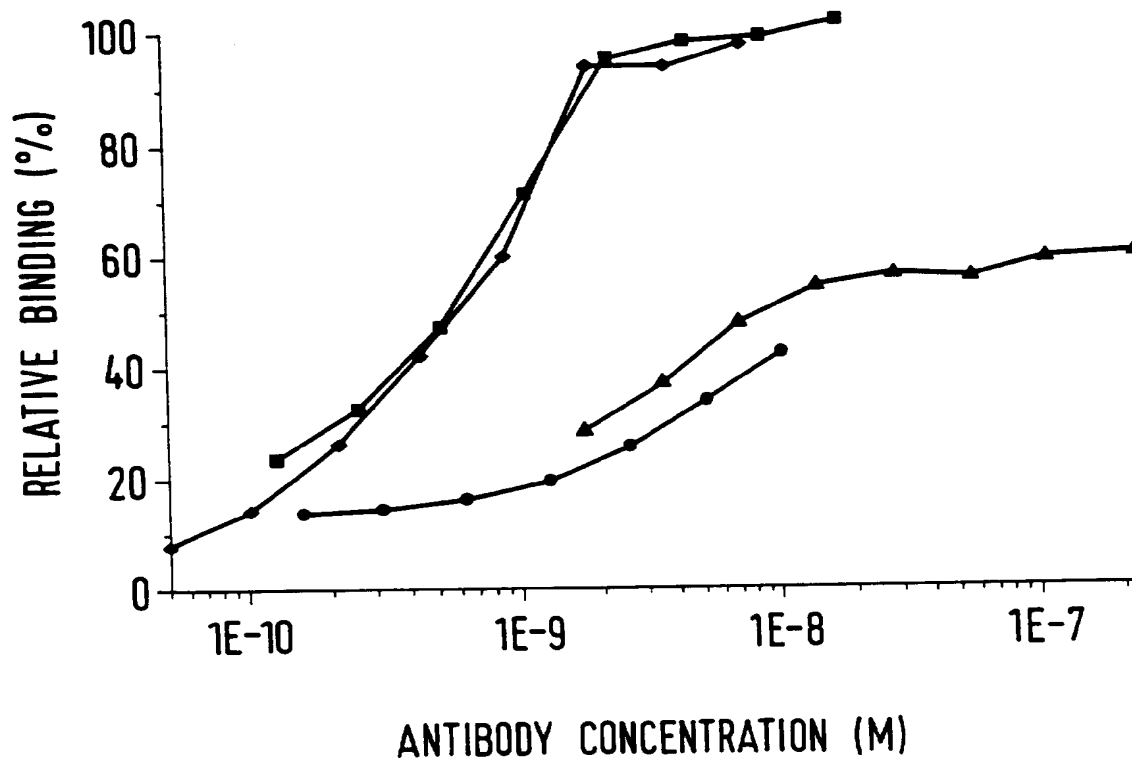
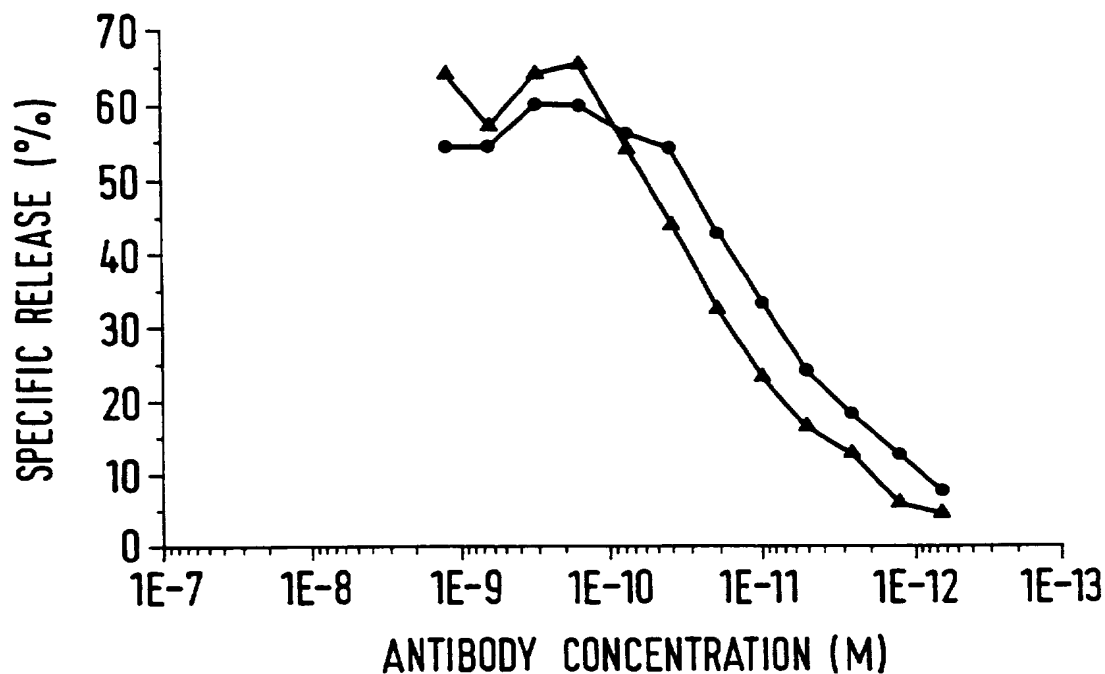
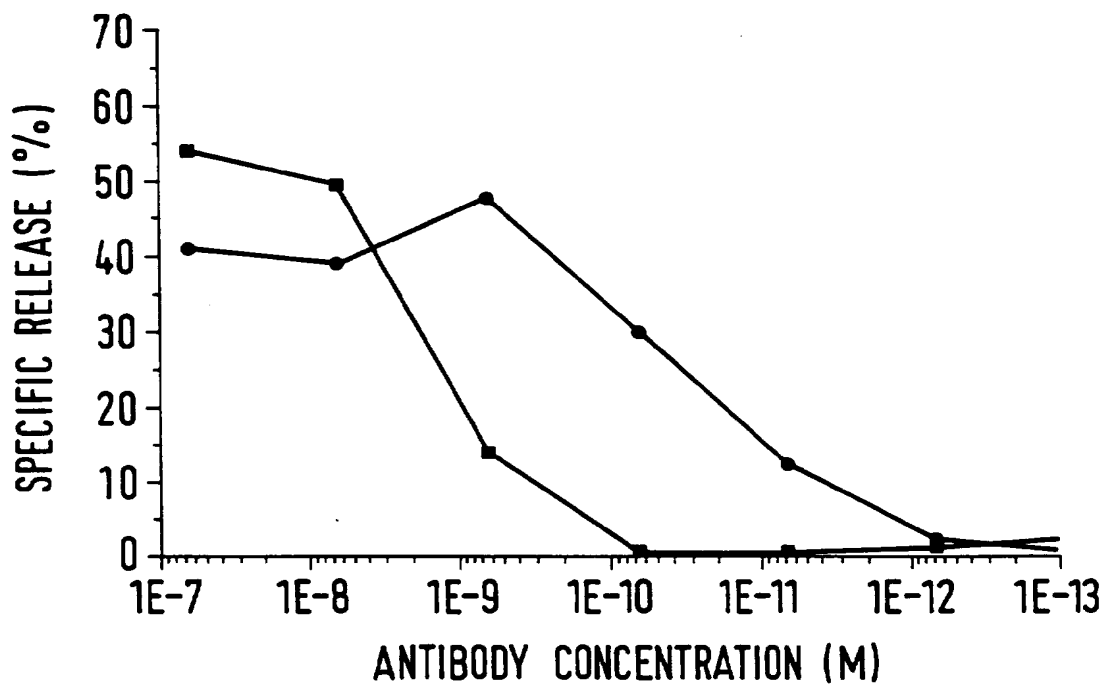
EFFECT OF VARIOUS HEAVY CHAIN FRAMEWORK SUBSTITUTIONS ON  
RELATIVE BINDING AFFINITY OF ANT-CD38 ANTIBODIES

Fig. 7

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EFFECT OF VARIOUS HEAVY CHAIN FRAMEWORK SUBSTITUTIONS ON  
ANTIBODY-DEPENDENT CELLULAR CYTOTOXICITY MEDICATED  
BY CD38 ANTIBODIES

*Fig. 8*

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/GB 95/02777

**A. CLASSIFICATION OF SUBJECT MATTER**  
IPC 6 C07K16/46 C07K16/28 A61K39/395

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JOURNAL OF MOLECULAR BIOLOGY, vol. 235, no. 1, 7 January 1994 LONDON, GB, pages 53-60, XP 000564648 A. CORTI ET AL. 'Idiotope determining regions of a mouse monoclonal antibody and its humanized versions.'	1-5,7
Y	see the whole document	9
Y	WO,A,94 17184 (SCHERING CORPORATION ET AL.) 4 August 1994 see examples see claims	9
	--- -/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

\* Special categories of cited documents :

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Date of the actual completion of the international search

27 March 1996

Date of mailing of the international search report

23.04.96

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Fax: (+ 31-70) 340-3016

Authorized officer

Nooij, F

## INTERNATIONAL SEARCH REPORT

Int'l Application No  
PCT/GB 95/02777

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO,A,94 13805 (CELLTECH LTD.) 23 June 1994  see page 12, line 19 - page 13, line 5 see example 1 see claims ---	1,3,4,7, 8,13,14, 16,18
X	WO,A,91 09967 (CELLTECH LTD.) 11 July 1991  see table 2 see examples see claims ---	1,3,5,7, 13-18
X	WO,A,94 09136 (KETTOCK LODGE, CAMPUS 2) 28 April 1994 see claims ---	1,3,5,7, 13
X	JOURNAL OF MOLECULAR BIOLOGY, vol. 224, no. 2, 20 March 1992 LONDON, GB, pages 487-499, XP 000564649 J. FOOTE ET AL. 'Antibody framework residues affecting the conformation of the hypervariable loops.' see abstract see table 2 ---	1,3,5-7, 11,13
X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 89, no. 10, 15 May 1992 WASHINGTON, DC, USA, pages 4285-4289, XP 000275844 P. CARTER ET AL. 'Humanization of an anti-p185HER2 antibody for human cancer therapy.' see abstract see table 1 ---	1,3,5,7, 13-18
A	EP,A,0 481 790 (THE WELLCOME FOUNDATION) 22 April 1992 see claims ---	1-18
P,X	THE JOURNAL OF IMMUNOLOGY, vol. 155, no. 2, 15 July 1995 BALTIMORE, MD, USA, pages 925-937, J. ELLIS ET AL. 'Engineered anti-CD38 monoclonal antibodies for immunotherapy of multiple myeloma.' see the whole document ---	1-18
	---	

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 95/02777

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,0, X	IMMUNOLOGY, vol. 83, suppl. 1, 5 - 7 December 1994 OXFORD, GB, page 70 XP 000565931 J. ELLIS ET AL. 'Characterisation of a humanised monoclonal anti-CD38 antibody.' see abstract -----	1-18



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/GB95/02777

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 14, 15  
because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claims 14 and 15 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No  
PCT/GB 95/02777

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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## INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/GB 95/02777

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